

```
FEATURES:
           1-210
5'UTR:
Start Codon: 211
Stop Codon: 1009
3'UTR:
           1012
5' UTR ANALYSIS:
Query=cDNA clone
Sbjct: genomic sequence
5' UTR Exon 1, non-coding
Score = 58.0 bits (29), Expect = 2e-10
Identities = 29/29 (100%)
Strand = Plus / Plus
Query: 1
          ggcgtcgccgcgggggagaaagaagccg 29
          1111111111111111111111111111111
Sbjct: 1535 ggcgtcgccgcgcggggagaaagaagccg 1563
5' UTR Exon 2, non-coding
Score = 349 bits (176), Expect = 3e-98
Identities = 176/176 (100%)
Strand = Plus / Plus
Query: 26
          qccqcqcccaqcccqqcqtcccqaqcaqcqcaggggaggatccccgcgcagtgacccggg 85
          Sbjct: 2001 gccgcgcccagcccggcgtcccgagcagcgagggaggatccccgcgcagtgacccggg 2060
          agccaccacagactctgggaggctcggcggctggagcagcagcagctccccgcagctcc\ 145
Query: 86
          Query: 146 cggcgcttccaggcagctctctgagccgtgccagaggcccggcccgccattcccag 201
          Sbjct: 2121 cggcgcttccaggcagctctctgagccgtgccagaggcccggccattcccag 2176
Score = 563 \text{ bits } (284), \text{ Expect} = e-162
Identities = 284/284 (100%)
Strand = Plus / Plus
5' UTR Exon 3, Protein coding region begins at nucleotide 211
Query: 199 cagccccgagccatgatgaagactttgtccagcgggaactgcacgctcagtgtgcccgcc 258
          Sbjct: 7474 cageceegageeatgatgaagaetttgteeagegggaaetgeacgeteagtgtgeeegee 7533
Homologous proteins:
Top BLAST Hits
                                                          Score
CRA|18000005194969 /altid=gi|10047088 /def=ref|NP 055125.1| sim...
                                                           538
                                                               e-152
CRA|18000005238449 /altid=gi|5059122 /def=gb|AAD38928.1|AF13440...
                                                           512 e-144
CRA|332000009620725 /altid=gi|8118457 /def=gb|AAF72997.1|AF2620...
                                                           342 2e-93
CRA|18000005232775 /altid=gi|7706359 /def=ref|NP_057168.1| ras-...
                                                           342 2e-93
CRA|8700000006130 /altid=gi|7230768 /def=gb|AAF43090.1|AF23915...
                                                           342 3e-93
CRA|18000005090459 /altid=gi|6677673 /def=ref|NP_033052.1| RAS,...
                                                           341 6e-93
CRA|89000000197633 /altid=gi|7295299 /def=gb|AAF50620.1| (AE003...
                                                           228 8e-59
CRA|105000014645240 /altid=gi|10503969 /def=gb|AAG17979.1|AF177...
                                                           214 1e-54
```

BLAST dbEST hits: gi|9345313 /dataset=dbest /taxon=960... 880 0.0 gi|9335874 /dataset=dbest /taxon=960... 846 0.0 gi|10143211 /dataset=dbest /taxon=96... 821 0.0 gi|9335309 /dataset=dbest /taxon=960... 813 0.0 gi|9150610 /dataset=dbest /taxon=9606... 662 0.0 gi|10144589 /dataset=dbest /taxon=960... 617 e-174 gi|9333908 /dataset=dbest /taxon=960... 599 e-169

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits: gi|9345313 Placenta choriocarcinoma gi|9335874 Uterus endometrium adenocarcinoma gi|10143211 Skin melanotic melanoma gi|9335309 Uterus endometrium adenocarcinoma gi|9150610 Skin melanotic melanoma qi|10144589 Skin melanotic melanoma

gi|9333908 Uterus endometrium adenocarcinoma

Expression information from PCR-based tissue screening panels:

Human fetal whole brain

- 1 MMKTLSSGNC TLSVPAKNSY RMVVLGASRV GKSSIVSRFL NGRFEDQYTP 51 TIEDFHRKVY NIRGDMYQLD ILDTSGNHPF PAMRRLSILT GDVFILVFSL
- 101 DNRESFDEVK RLQKQILEVK SCLKNKTKEA AELPMVICGN KNDHGELCRQ
- 151 VPTTEAELLV SGDENSAYFE VSAKKNTNVD EMFYVLFSMA KLPHEMSPAL
- 201 HRKISVQYGD AFHPRPFCMR RVKEMDAYGM VSPFARRPSV NSDLKYIKAK
- 251 VLREGQARER DKCTIQ

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION N-glycosylation site

Number of matches: 2

- 1 9-12 NCTL
- 2 125-128 NKTK
- [2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 4

- 1 84-87 RRLS
- 2 174-177 KKNT
- 3 202-205 RKIS
- 4 236-239 RRPS
- [3] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

Number of matches: 2

- 1 19-21 SYR
- 2 172-174 SAK
- [4] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

Number of matches: 5

- 1 51-54 TIED
- 2 105-108 SFDE
- 3 154-157 TEAE
- 4 161-164 SGDE
- 5 177-180 TNVD
- [5] PDOC00007 PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site

220-228 RRVKEMDAY

[6] PDOC00266 PS00294 PRENYLATION Prenyl group binding site (CAAX box)

263-266 CTIQ

[7] PDOC00016 PS00016 RGD Cell attachment sequence

63-65 RGD '

[8] PDOC00017 PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop)

26-33 GASRVGKS

BLAST Alignment to Top Hit:

Score = 538 bits (1372), Expect = e-152 Identities = 265/266 (99%), Positives = 265/266 (99%)

Query: 1 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY

Sbjct: 13 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 72

Query: 61 NIRGDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120 NIRGDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK

Sbjct: 73 NIRGDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 132

Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSAKKNTNVD 180 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDEN AYFEVSAKKNTNVD

Sbjct: 133 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENCAYFEVSAKKNTNVD 192

Query: 181 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 240 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV

Sbjct: 193 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 252

Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266
NSDLKYIKAKVLREGQARERDKCTIQ
Sbjct: 253 NSDLKYIKAKVLREGQARERDKCTIQ 278

Complete Amino Acid Sequence of gi|10047088 /def=ref|NP_055125.1| similar to mouse Ras, dexamethasone-induced 1; tumor endothelial marker 2 [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=278

Length = 278
NOTE: UNDERLINED RESIDUES NOT PRESENT IN THE PROTEIN OF THE PRESENT INVENTION

1 mpaslallqp rammktlssg nctlsvpakn syrmvvlgas rvgkssivsr flngrfedqy

61 tptiedfhrk vynirgdmyg ldildtsgnh pfpamrrlsi ltgdvfilvf sldnresfde

121 vkrlqkqile vksclknktk eaaelpmvic gnkndhgelc rqvptteael lvsgdencay

181 fevsakkntn vdemfyvlfs maklphemsp alhrkisvqy gdafhprpfc mrrvkemday

241 gmvspfarrp svnsdlkyik akvlregqar erdkctiq

Score = 512 bits (1304), Expect = e-144 Identities = 252/266 (94%), Positives = 256/266 (95%)

Query: 1 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60 MMKTLSSGNCTL+VPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY

Sbjct: 1 MMKTLSSGNCTLNVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60

Query: 61 NIRGDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120 NI GDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLD+RESFDEVKRLQKQILEVK

Sbjct: 61 NIHGDMYQLDILDTSGNHPFPAMRRLSILTGDVFILVFSLDSRESFDEVKRLQKQILEVK 120

Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSAKKNTNVD 180 SCLKNKTKEAAELPMVICGNKNDH ELCRQVP EAELLVSGDEN AYFEVSAKKNTNV+

Sbjct: 121 SCLKNKTKEAAELPMVICGNKNDHSELCRQVPAMEAELLVSGDENCAYFEVSAKKNTNVN 180

Query: 181 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 240

EMFYVLFSMAKLPHEMSPALH KISVQYGDAFHPRPFCMRR K AYGMVSPFARRPSV

Sbjct: 181 EMFYVLFSMAKLPHEMSPALHHKISVQYGDAFHPRPFCMRRTKVAGAYGMVSPFARRPSV 240

Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266

NSDLKYIKAKVLREGQARERDKC+IQ

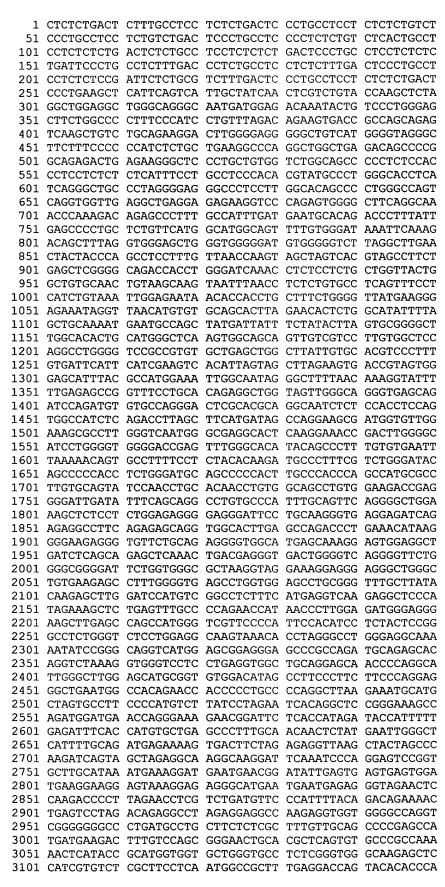
Sbjct: 241 NSDLKYIKAKVLREGQARERDKCSIQ 266

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	126.2	2.8e-36	1
CE00060	CE00060 rab ras like	20.7	0.00013	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value
CE00060	1/2	22	52	 26	56		16.9	0.0014
CE00060	2/2	162	183	 159	181		3.3	7.5
PF00071	1/1	21	186	 1	169	[.	126.2	2.8e-36



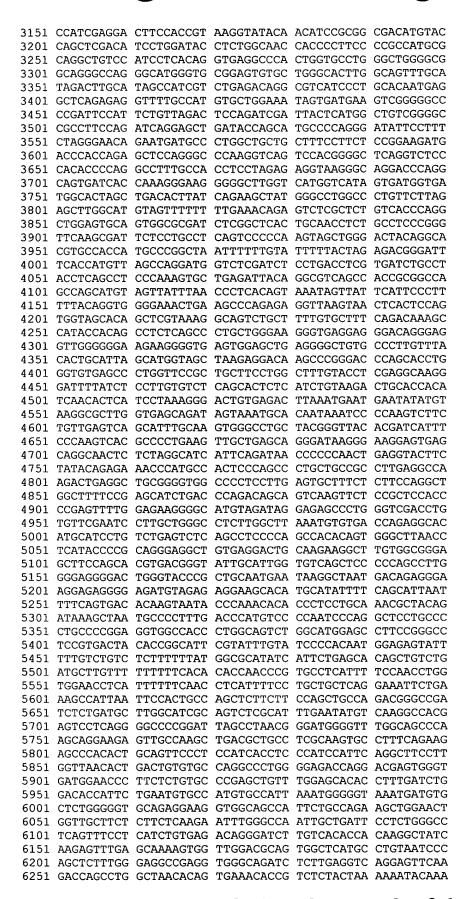
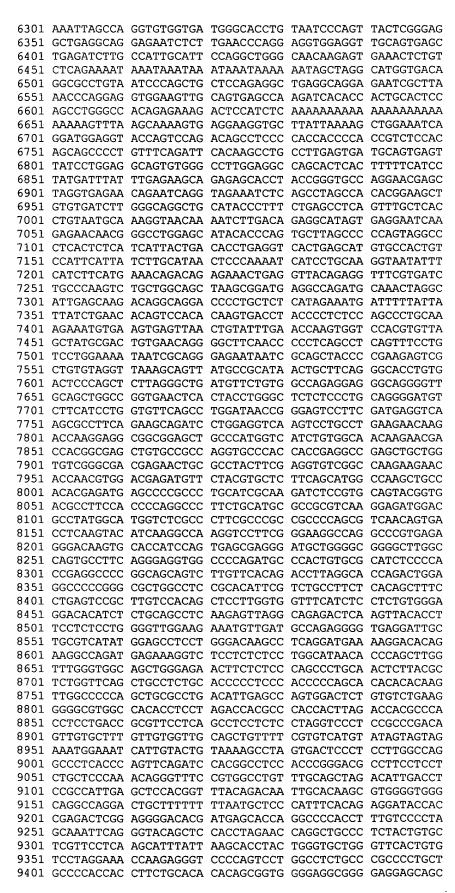
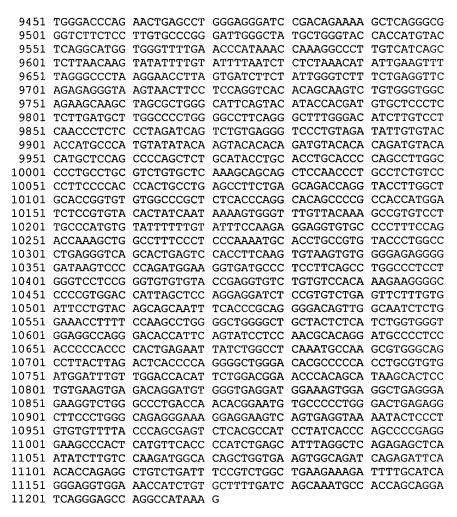


FIGURE 3, page 2 of 6





FEATURES:

Start: 3000 Exon: 3000-3270 Intron: 3271-7693 Exon: 7694-8220

Stop: 8221

CHROMOSOME MAP POSITION:

Chromosome 22

ALLELIC VARIANTS (SNPs):

DNA			
Position	Major	Minor	Domain
3951	С	Т	Intron
4127	С	T	Intron
4157	G	A	Intron
4513	С	T	Intron
6894	С	A	Intron
8409	G	С	Beyond ORF(3')
8437	T	G	Beyond ORF(3')
8579	T	C	Beyond ORF(3')
10292	A	G	Beyond ORF(3')
10792	A	G	Beyond ORF(3')

Context:

DNA Position

3951

GTGCCACCATGCCCGGCTAATTTTTTGTATTTTTACTAGAGACCGGGATTTCACCATGTTA
GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCTACCTCAGCCTCCCAAAGTGCT
GAGATTACAGGCGTCAGCCACCGCGGCCAGCCAGCATGTAGTTATTTAACCCTCACAGTA
AATAGTTATTCATTCCCTTTTTACAGGTGGGGAAACTGAAGCCCAGAGAGGTTAAGTAAC
TCACTCCAGTGGTAGCACAGCTCGTAAAGGCAGTCTGCTTTTGTGCTTTCAGACAAAGCC

4127

AGTAATAGTTATTCATTCCCTTTTTACAGGTGGGGAAACTGAAGCCCAGAGAGGTTAAG TAACTCACTCCAGTGGTAGCACAGCTCGTAAAGGCAGTCTGCTTTTGTGCTTTCAGACAA AGCCATACCACAGCCTCTCAGCCCTGCTGGGAAGGGTGAGGAGGGACAGGGAGGTTGGGG GGAAGAAGGGGTGAGTGGAGCTGAGGGGCTGTGCCCTTGTTTACACTGCATTAGCATGGT AGCTAAGAGGACAAGCCCGGGACCCAGCACCTGGGTGTGAGCCCTGGTTCCGCTGCTTCC

4157

4513

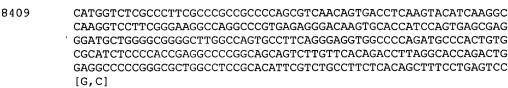
TCGTAAAGGCAGTCTGCTTTTGTGCTTTCAGACAAAGCCATACCACAGCCTCTCAGCCCT GCTGGGAAGGGTGAGGAGGACAGGGAGGTTGGGGGGAAGAAGGGGTGAGTGGAGCTGAG GGGCTGTGCCCTTGTTTACACTGCATTAGCATGGTAGCTAAGAGGACAAGCCCGGGACCC AGCACCTGGGTGTGAGCCCTGGTTCCGCTGCTTCCTGGCTTTTGTACCTCGAGGCAAGGGA TTTTATCTCCTTGTGTCTCAGCACTCTCATCTGTAAGACTGCACCACATCAACACTCATC [C,T]

TAAAGGGACTGTGAGACTTAAATGAATGAATATATGTAAGGCGCTTGGTGAGCAGATAGT AAATGCACAATAAATCCCCAAGTCTTCTGTTGAGTCAGCATTTGCAAGTGGGCCTGCTAC GGGTTACACGATCATTTCCCAAGTCACCCCCTGAAGTTGCTGAGCAGGGATAAGGGAAG GAGTGAGCAGCAACTCTCTAGGCATCATTCAGATAACCCCCCAACTGAGGTACTTCTAT ACAGAGAAACCCATGCCACTCCCAGCCCTGCTGCCGCCTTGAGGCCAAGACTGAGGCTGC

6894

ACGAGCTAGGTGAGAACAGAATCAGGTAGAAATCTCAGCCTAGCCACACGGAAGCTGTGT GATCTTGGGCAGGCTGCATACCCTTTCTGAGCCTCAGTTTGCTCACCTGTAATGCAAAGG TAACAAAATCTTGACAGAGGCATAGTGAGGGAATCAAGAGAACAACGGGCCTGGAGCATAC ACCCAGTGCTTAGCCCCCAGTAGGCCCTCACTCTCATCATTACTGACACCTGAGGTCACT GAGCATGTGCCACTGTCCATTCATTATCTTGCATAACTCCCAAAATCATCCTGCAAGGTA 8579

10292



GCCCACTGTGCGCATCTCCCCACCGAGGCCCCGGCAGCAGTCTTGTTCACAGACCTTAGG CACCAGACTGGAGGCCCCCGGGCGCTGGCCTCCGCACATTCGTCTGCCTTCTCACAGCTT TCCTGAGTCCGCTTGTCCACAGCTCCTTGGTGGTTTCATCTCTCTGTGGGAGGACACAT CTCTGCAGCCTCAAGAGTTAGGCAGAGACTCAAGTTACACCTTCCTCTCTGGGGTTGGA AGAAATGTTGATGCCAGAGGGGTGAGGATTGCTGCGTCATATGGAGCCTCCTGGGACAAG [T,C]

AGCCTTGGCCCTGCCTGCGTCTGTGCTCAAAGCAGCTCCAACCCTGCCTCTGTCCC CTTCCCCACCCACTGCCTGAGCCTTCTGAGCAGACCAGGTACCTTGGCTGCACCGGTGTG TGGCCCGCTCTCACCCAGGCACAGCCCCGCCACCATGGATCTCCGTGTACACTATCAATA AAAGTGGGTTTGTTACAAAGCCGTGTCCTTGCCCATGTGTATTTTTTTGTATTTCCAAGAG GAGGTGTGCCCCTTTCCAGACCAAAGCTGGCCTTTCCCCCAAAATGCACCTGCCGTGT [A, G]

CCCTGGCCCTGAGGGTCAGCACTGAGTCCACCTTCAAGTGTAAGTGTGGGGAGAGGGGGA TAAGTCCCCCAGATGGAAGGTGATGCCCTCCTTCAGCCTGGCCCTCCTGGGTCCTCCGGG TGTGTGTACCGAGGTGTCTGTGTCCACAAAGAAGGGGCCCCCGTGGACCATTAGCTCCAG GAGGATCTCCGTGTCTGAGTTCTTTGTGATTCCTGTACAGCAGCAATTTCACCCGCAGGG GACAGTTGGCAATCTCTGGAAACCTTTTCCAAGCCTGGGGCTGGGGCTGCTACTCTCATC

> AGCACTCCTGTGAAGTGAGACAGGATGTGGGTGAGGATGGAAAGTGGAGGCTGAGGGAGA AGGTCTGGGCCCTGACCAACACGGAATGTGCCCCCTGGGACTGAGAGGCTTCCCTGGGCA GAGGGAAAGGAGGAAGTCAGTGAGGTAAAATACTCCCTGTGTTTTTACCCAGCGAGTCT CACGCCATCCTATCACCCAGCCCCGAGGGAAGCCCACTCATGTTCACCCCATCTGAGCAT TTAGGCTCAGAGAGCTCAATATCTTGTCCAAGATGGCACAGCTGGTGAAGTGGCAGATCA

FIGURE 3, page 6 of 6